

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/509,779

1642

DATE: 02/01/2001  
TIME: 21:16:57

INPUT SET: S36345.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

RECEIVED

FEB 05 2001

TECH CENTER 1600 2350

## SEQUENCE LISTING

## (1) General Information:

## (i) APPLICANT:

~~(A) NAME: Yi Sun~~  
~~(B) STREET: 4841 Hillway Court~~  
~~(C) CITY: Ann Arbor~~  
~~(D) STATE: Michigan~~  
~~(E) COUNTRY: USA~~  
~~(F) POSTAL CODE (ZIP): 48105~~  
~~(G) TELEPHONE: (313) 996-1959~~  
~~(H) TELEFAX: (313) 996-7158~~

Does Not Comply  
Corrected Diskette Needed

delete

must be on  
same line as headinginsert these  
MANDATORY  
headings and  
their

(ii) TITLE OF INVENTION: Sensitive to Apoptosis Gene (SAG)

(iii) NUMBER OF SEQUENCES: 50

## (v) (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE:  
(B) STREET:  
(C) CITY:  
(D) STATE:  
(E) COUNTRY:  
(F) ZIP:

responses  
for a U.S.  
case

(vii) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:

insert these mandatory headings

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1140 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

FYI: EPO format  
is invalid  
for U.S. cases

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 17..355

## (ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 17..355

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

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(B) LOCATION: 1..1140  
(D) OTHER INFORMATION: /note= "Mouse SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

47  
48  
49  
50  
51  
52  
53 GTTCTGCGCC GCCGCC ATG GCC GAC GTG GAG GAC GGC GAG GAA CCC TGC 49  
54 Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys  
55 1 5 10  
56  
57 GTC CTT TCT TCG CAC TCC GGG AGC GCA GGC TCC AAG TCG GGA GGC GAC 97  
58 Val Leu Ser Ser His Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp  
59 15 20 25  
60  
61 AAG ATG TTC TCT CTC AAG AAG TGG AAC GCG GTA GCC ATG TGG AGC TGG 145  
62 Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp  
63 30 35 40  
64 GAC GTT GAG TGC GAT ACC TGT GCC ATC TGC AGG GTC CAG GTG ATG GAT 193  
65 Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp  
66 45 50 55  
67  
68 GCC TGC CTT CGA TGT CAA GCT GAA AAC AAG CAA GAG GAC TGT GTT GTG 241  
69 Ala Cys Leu Arg Cys Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val  
70 60 65 70 75  
71  
72 GTC TGG GGA GAG TGT AAC CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG 289  
73 Val Trp Gly Glu Cys Asn His Ser Phe His Asn Cys Cys Met Ser Leu  
74 80 85 90  
75  
76 TGG GTG AAA CAG AAC AAT CGC TGC CCT CTG TGC CAG CAG GAC TGG GTA 337  
77 Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val  
78 95 100 105  
79  
80 GTC CAA AGA ATC GGC AAA TGAGAGGTGG CCCAGGCGCT CCTGGTGTGG 385  
81 Val Gln Arg Ile Gly Lys  
82 110  
83  
84 TTGCTGACCC TGGACAAAGA CTAAACACTG CAGGGGATTC ATCCTTGAGA GAGAGAGGAT 445  
85  
86 GCTGTGCGCC TTTGAGACTC ACCAAAGGCT TGCTTTATTA ATTTGTCTGT TTAGTTTTGG 505  
87  
88 GAAATTCTCT ACAATTAAGA TAATTTGTGA AAAATGGCCT TTCCTACCTC TGGTGTGTGT 565  
89  
90 GTGTGATACG AATGCATAGA AGAGCGAGAA CACCAGAAAA TGATCTTTGT TTATCTGTAC 625  
91  
92 CCACGACTGG AACATTGTGT TCACAGAAGA ACATTGTTTG TGTTTATGCT TGAGGGTTAA 685  
93  
94 AAAATAGATA AACGAATGTT ACAGTAACAA ATAAAATGCA TTGAAAAGCC GACTCCTCCT 745  
95  
96 AATCCTTTTT GTGTTGGGAG AGAGGCAAGC GAGGCCACCC TGCTGTCTTC ATTTGCTGTG 805  
97  
98 AATGAGGATT TTAACCTGCA CTCAGTGAAG AGGCGTAACT GTCGGGTAAA CTGTAATATG 865  
99

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100 GCGTAACTGT CGGGTAAACG GCTTTGTCTC CTGACTTCTC CATCTTTGAC TTGGCCAGGA 925  
101  
102 AGCCTGGATT GTTCAACCAC TTAGTTCTAA AGAACTGTTT TCTGTTTTTTG CCGAAGGTTG 985  
103  
104 TATTGTATGT TTTAGTCAAA AATATTAGTA GGAAAATGGC TTACTAGTAT AACACTGAAG 1045  
105  
106 TTCATTATGC AATGTTTTAA TAAAATATTG TGCTTTGAGT TATTAAAGTT TGATATATAC 1105  
107  
108 TCTTAAATC ATTAACTAA TTCATCAATT AAATG 1140  
109  
110

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

121 Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys Val Leu Ser Ser His  
122 1 5 10 15  
123  
124 Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu  
125 20 25 30  
126  
127 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp  
128 35 40 45  
129  
130 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys  
131 50 55 60  
132  
133 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys  
134 65 70 75 80  
135  
136 Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn  
137 85 90 95  
138  
139 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly  
140 100 105 110  
141  
142 Lys  
143  
144

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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153 (ii) MOLECULE TYPE: cDNA  
154  
155  
156 (ix) FEATURE:  
157 (A) NAME/KEY: CDS  
158 (B) LOCATION:1..339  
159  
160 (ix) FEATURE:  
161 (A) NAME/KEY: mat\_peptide  
162 (B) LOCATION:1..339  
163  
164 (ix) FEATURE:  
165 (A) NAME/KEY: misc\_feature  
166 (B) LOCATION:1..754  
167 (D) OTHER INFORMATION:/note= "Human SAG"  
168  
169  
170 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
171  
172 ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48  
173 Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His  
174 1 5 10 15  
175  
176 TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96  
177 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu  
178 20 25 30  
179  
180 AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT 144  
181 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp  
182 35 40 45  
183  
184 ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT 192  
185 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys  
186 50 55 60  
187  
188 CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT 240  
189 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys  
190 65 70 75 80  
191  
192 AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC 288  
193 Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn  
194 85 90 95  
195  
196 AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC 336  
197 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly  
198 100 105 110  
199  
200 AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGG 389  
201 Lys  
202  
203  
204 TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG 449  
205

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206 GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT 509  
207  
208 ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC 569  
209  
210 TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 629  
211  
212 GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGAAGCAGT TTCGAGACTT 689  
213  
214 TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT 749  
215  
216 TTAAA 754  
217  
218

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

228  
229 Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His  
230 1 5 10 15  
231  
232 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu  
233 20 25 30  
234  
235 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp  
236 35 40 45  
237  
238 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys  
239 50 55 60  
240  
241 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys  
242 65 70 75 80  
243  
244 Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn  
245 85 90 95  
246  
247 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly  
248 100 105 110  
249  
250 Lys  
251  
252

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/509,779**DATE: 02/01/2001  
TIME: 21:16:59*INPUT SET: S36345.raw*

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Yi Sun
7	Unknown or Misplaced Identifier	(B) STREET: 4841 Hillway Court
8	Unknown or Misplaced Identifier	(C) CITY: Ann Arbor
9	Unknown or Misplaced Identifier	(D) STATE: Michigan
10	Unknown or Misplaced Identifier	(E) COUNTRY: USA
11	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 48105
12	Unknown or Misplaced Identifier	(G) TELEPHONE: (313) 996-1959
13	Unknown or Misplaced Identifier	(H) TELEFAX: (313) 996-7158

PAGE: 1

**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/09/509,779**

DATE: 02/01/2001  
TIME: 21:16:59

*INPUT SET: S36345.raw*

ADDRESSEE  
STREET  
CITY  
STATE  
COUNTRY  
ZIP  
CORRESPONDENCE ADDRESS  
APPLICATION NUMBER  
FILING DATE  
CLASSIFICATION  
CURRENT APPLICATION DATA  
APPLICATION NUMBER  
FILING DATE  
PRIOR APPLICATION DATA